

Nucleotide and Amino Acid Sequence of AIM-I

-51	GGCACGAGCGGCTGCCTGGCTGACTTACAGCAGTCAGACTCTGACAGGTTCA	8
-16	CCGTGCTCGCCGACGGACCGACTGAATGTCGTCAGTCTGAGACTGTCCAAGTACCGATAC	3
	M A M	
9	ATGGAGGTCCAGGGGGGACCCAGCCTGGGACAGACCTGCGTGCTGATCGTGATCTTCACA	68
4	TACCTCCAGGTCCCCCTGGGTGCGACCGTGTCTGGACGCACGACTAGCACTAGAAGTGT	23
	M E V Q G G P S L G Q T C V L I V I F T	
69	GTGCTCCTGCAGTCTCTCTGTGTGGCTGTAACCTACGTGTACTTTACCAACGAGCTGAAG	128
24	CACGAGGACGTCAGAGAGACACACCGACATTGAATGCACATGAAATGGTTGCTCGACTTC	43
	V L L Q S L C V A V T Y V Y F T N E L K	
129	CAGATGCAGGACAAGTACTCCAAAAGTGGCATTGCTTGTTTCTTAAAAGAAGATGACAGT	188
44	GTCTACGTCCTGTTTCATGAGGTTTTACCGTAACGAACAAAGAATTTTCTTCTACTGTCA	63
	Q M Q D K Y S K S G I A C F L K E D D S	
189	TATTGGGACCCCAATGACGAAGAGAGTATGAACAGCCCCTGCTGGCAAGTCAAGTGGCAA	248
64	ATAACCCTGGGGTTACTGCTTCTCTCATACTTGTGCGGGGACGACCGTTCAGTTCACCGTT	83
	Y W D P N D E E S M N S P C W Q V K W Q	
249	CTCCGTCAGCTCGTTAGAAAGATGATTTTGAGAACCTCTGAGGAAACCATTTCTACAGTT	308
84	GAGGCAGTCGAGCAATCTTTCTACTAAACTCTTGGAGACTCCTTTGGTAAAGATGTCAA	103
	L R Q L V R K M I L R T S E E T I S T V	
309	CAAGAAAAGCAACAAAATATTTCTCCCCTAGTGAGAGAAAGAGGTCCTCAGAGAGTAGCA	368
104	GTTCTTTTCGTTGTTTTATAAAGAGGGGATCACTCTCTTCTCCAGGAGTCTCTCATCGT	123
	Q E K Q Q N I S P L V R E R G P Q R V A	
369	GCTCACATAACTGGGACCAGAGGAAGAAGCAACACATTGTCTTCTCCAAACTCCAAGAAT	428
124	CGAGTGTATTGACCCTGGTCTCCTTCTTCGTTGTGTAACAGAAGAGGTTTGAGGTTCTTA	143
	A H I T G T R G R S N T L S S P N S K N	
429	GAAAAGGCTCTGGGCCGAAAATAAACTCCTGGGAATCATCAAGGAGTGGGCATTTCATTC	488
144	CTTTTCCGAGACCCGGCGTTTTATTGAGGACCCTTAGTAGTTCCTCACCCGTAAGTAAG	163
	E K A L G R K I N S W E S S R S G H S F	

FIG.1A

CTGAGCAACTTGCACTTGAGGAATGGTGAAGTGGTCATCCATGAAAAAGGGTTTTACTAC
 489 -+-----+-----+-----+-----+-----+-----+-----+----- 548
 GACTCGTTGAACGTGAAGTCTTACCACTTGACCAGTAGGTACTTTTTCCCAAAATGATG
 164 L S N L H L R N G E L V I H E K G F Y Y 183
 ATCTATTTCCCAACATACTTTTCGATTTTCAGGAGGAAATAAAAGAAAACACAAAGAACGAC
 549 -+-----+-----+-----+-----+-----+-----+-----+----- 608
 TAGATAAGGGTTTGTATGAAAGCTAAAGTCTCCTTTATTTTCTTTTGTGTTTCTTGCTG
 184 I Y S Q T Y F R F Q E E I K E N T K N D 203
 AAACAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCCTATATTGTTGATG
 609 -+-----+-----+-----+-----+-----+-----+-----+----- 668
 TTTGTTTACCAGGTTATATAAATGTTTATGTGTTCAATAGGACTGGGATATAACAACCTAC
 204 K Q M V Q Y I Y K Y T S Y P D P I L L M 223
 AAAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCCATCTAT
 669 -+-----+-----+-----+-----+-----+-----+-----+----- 728
 TTTTCACGATCTTTATCAACAACCAGATTTCTACGTCTTATACCTGAGATAAGGTAGATA
 224 K S A R N S C W S K D A E Y G L Y S I Y 243
 CAAGGGGGAATATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTCTGTAACAAATGAG
 729 -+-----+-----+-----+-----+-----+-----+-----+----- 788
 GTTCCCCCTTATAAACTCGAATTCCTTTTACTGTCTTAAAAACAAAGACATTGTTTACTC
 244 Q G G I F E L K E N D R I F V S V T N E 263
 CACTTGATAGACATGGACCATGAAGCCAGTTTTTTTCGGGGCCTTTTGTAGTTGGCTAACTG
 789 -+-----+-----+-----+-----+-----+-----+-----+----- 848
 GTGAAGTATCTGTACCTGGTACTTCGGTCAAAAAAGCCCCGGAAAAATCAACCGATTGAC
 264 H L I D M D H E A S F F G A F L V G 281
 ACCTGGAAAGAAAAAGCAATAACCTCAAAGTGACTATTTCAGTTTTTCAGGATGATACACTA
 849 -+-----+-----+-----+-----+-----+-----+-----+----- 908
 TGGACCTTTCTTTTTCGTTATTGGAGTTTCACTGATAAGTCAAAAGTCCTACTATGTGAT
 TGAAGATGTTTCAAAAAATCTGACCAAAACAAACAAACAGAAAAACAGAAAAACAAAAAAC
 909 -+-----+-----+-----+-----+-----+-----+-----+----- 968
 ACTTCTACAAAGTTTTTGTAGTGGTTTTGTTTGTCTTTTGTCTTTTGTCTTTTGTCTTTTGT
 CTCTATGCAATCTGAGTAGAGCAGCCACAACCAAAAAATTCTACAACACACACTGTTCTG
 969 -+-----+-----+-----+-----+-----+-----+-----+----- 1028
 GAGATACGTTAGACTCATCTCGTCGGTGTGGTTTTTTAAGATGTTGTGTGTGACAAGAC
 AAAGTGACTCACTTATCCCAAGAAAATGAAATTGCTGAAAGATCTTTCAGGACTCTACCT
 1029 -+-----+-----+-----+-----+-----+-----+-----+----- 1088
 TTTCACTGAGTGAATAGGGTTCTTTTACTTTAACGACTTTCTAGAAAGTCTGAGATGGA
 CATATCAGTTTGCTAGCAGAAATCTAGAAGACTGTCAGCTTCCAAACATTAATGCAATGG
 1089 -+-----+-----+-----+-----+-----+-----+-----+----- 1148
 GTATAGTCAAACGATCGTCTTTAGATCTTCTGACAGTCGAAGGTTTGTAAATTACGTTACC

FIG. 1B

[illegible]

FIG. 1C

Alignment of AIM-I to Human Fas Ligand
(Similarity = 48.594 % Identity = 22.892 %)

```

4 MEVQGGPSLGQTCVLIVFTVL.....LQSLCVAVTYV 36
  :: ..... | : |.....
15 vdssasspwappgtvlpcptsvprpgrpppppppppppppppppppplp 64
37 YFTNELKQMQDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQ 86
  :: |.....:..|. |:: : : : : |:: ::|..
65 plp..lpplkkrgnhstgcllvm..ffmvlvalvglglgmfql.fh|qk 109
87 LVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHITGTRGRSNTL 136
  : : : : ||: ... ||| . . . . |: . | .||:| |::|..
110 elaelrestsqmhtasslekqighpspppekkelrkvahlt...gksnsr 156
137 SSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYS 186
  | | ..... | :||.....|:||||:|. |:|::||
157 smplewedty.....givilsgvkykkgglvinetglyfvys 193
187 QTYFRFQEEIKENTKNDKQMVQYIYKYTS.YPDPILLMK$ARN$CWSKDA 235
  ..||| :.. |: : : : :|. | ||:.....|: . |: :...
194 kvyfr.....gqscnnlplshkvymrnsrypqlvmmegkmmsycttgq 237
236 EYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
  :: | | |:|:|...|::|. |: |:::.....||| : :
238 mwar.ssy|gavfnltsadhlyvnselslvnfeesqtffglykl 281

```

FIG.2

Alignment Report of AIM-1, hFas Ligand, TNF- α and TNF- β
by Clustal Method with PAM250 Residue Weight Table

	10	20	30	
1	M A M M E V Q G G P S L - - - - - G Q T C V L I V I F T V L	AIM 1		
1	M Q Q P M N Y P C P Q I F W V D S S A T I S S W A P P G S V F	FAS LIGAND		
1	M -	tnfa.pep		
1	M - T P P E R L F	tnfb.pep		
	40	50	60	
26	L Q S L C V A V T Y V Y F T N E L K Q M Q D K Y S K S G I A	AIM 1		
31	P C P S C G P R G - - - - - P D Q R R P P P P P P V S P L P	FAS LIGAND		
2	- S T E S M I R D V E	tnfa.pep		
9	L P R V C G T T -	tnfb.pep		
	70	80	90	
56	C F L K E D D S Y W D P N D E E S M N S P C W Q V K W Q L R	AIM 1		
57	- - P P S Q P L P L P L T P L K K K D H N T N L W L P V V	FAS LIGAND		
12	- - L A E E A L P - - - - - - - - - - K K T G G P Q G S R R C L	tnfa.pep		
17	- L W L L	tnfb.pep		
	100	110	120	
86	Q L V R K M I L R T S E E T I S T V Q E K Q Q N I S P L V R	AIM 1		
85	F F M V L V A L V G M G L G - M Y Q L F H L Q K E L A E L R	FAS LIGAND		
32	F L S L F S F L I V A G A T T L F C L L H F G V I G P Q R E	tnfa.pep		
21	L L G L L L V L - - - - - - - - - - - - - - - - L P G A Q	tnfb.pep		
	130	140	150	
116	E K G P Q R V A A H I T G T R G R S N T L S S P N S K N E K	AIM 1		
114	E F T - N Q S L K V S S F E K Q I A N P S T P S E K K E P R	FAS LIGAND		
62	E S P R D L S L I S P L A Q A V R S S S R T P S D - - - - K	tnfa.pep		
34	G L P - G V G L T P S A A Q T A R Q H P K M H L A H S T L K	tnfb.pep		
	160	170	180	
146	A L G R K I N S - - - - - - - - - - W E S S R S G H S F L S N	AIM 1		
143	S V A H L T G N P H S R S I P L E W E D T Y G T A L I - S G	FAS LIGAND		
88	P V A H V V A N P Q A E G Q - L Q W L N R R A N A L L A N G	tnfa.pep		
63	P A A H L I G D P - S K Q N S L L W R A N T D R A F L Q D C	tnfb.pep		

FIG.3A

	190	200	210	
167	L H L R N G K L V I H E K G F Y Y I Y S Q T Y F R F Q E E I			AIM 1
172	V K Y K K G G L V I N E T G L Y F V Y S K V Y F R G Q S C N			FAS LIGAND
117	V E L R D N Q L V V P S E G L Y L I Y S Q V L F K G Q S C -			tnfa.pep
92	F S L S N N S L L V P T S G I Y F V Y S Q V V F S C K A Y S			tnfb.pep
	220	230	240	
197	K E N T K N D K Q M V Q Y I Y K Y T S - Y P D P I L L M K S			AIM 1
202	N Q P - - - - - L N H K V Y M R N S K Y P E D L V L M E E			FAS LIGAND
146	- - - P S T H V L L T H T I S R I A V S Y Q T K V N L L S A			tnfa.pep
122	P K A P S S P L Y L A H E V Q L F S S Q Y P F H V P L L S S			tnfb.pep
	250	260	270	
226	A R N S C W S K D A E Y G L - - - - - Y S I Y Q G G I F E L			AIM 1
226	K R L N Y C - - - - - T T G Q I W A H S S Y L G A V F N L			FAS LIGAND
173	I K S P C Q R E T P E G A E A K P W Y E P I Y L G C V F Q L			tnfa.pep
152	Q K M V Y P - - - - - G L Q E P W L H S M Y H G A A F Q L			tnfb.pep
	280	290	300	
251	K E N D R I F V S V T N E H L I D K D H E A S - F F G A F L			AIM 1
250	T S A D H L Y V N I S Q L S L I N F E E S - K T F F G L Y -			FAS LIGAND
203	E K G D R L S A E I N R P D Y L D F A E S G Q V Y F G I I -			tnfa.pep
176	T Q G D Q L S T R T D G I P H L V L S P S - T V F F G A F -			tnfb.pep
	310	320	330	
280	V G -			AIM 1
278	- K L			FAS LIGAND
232	- A L			tnfa.pep
204	- A L			tnfb.pep

Decoration 'Decoration #1': Box residues that match the Consensus within 2 distance units.

FIG.3B

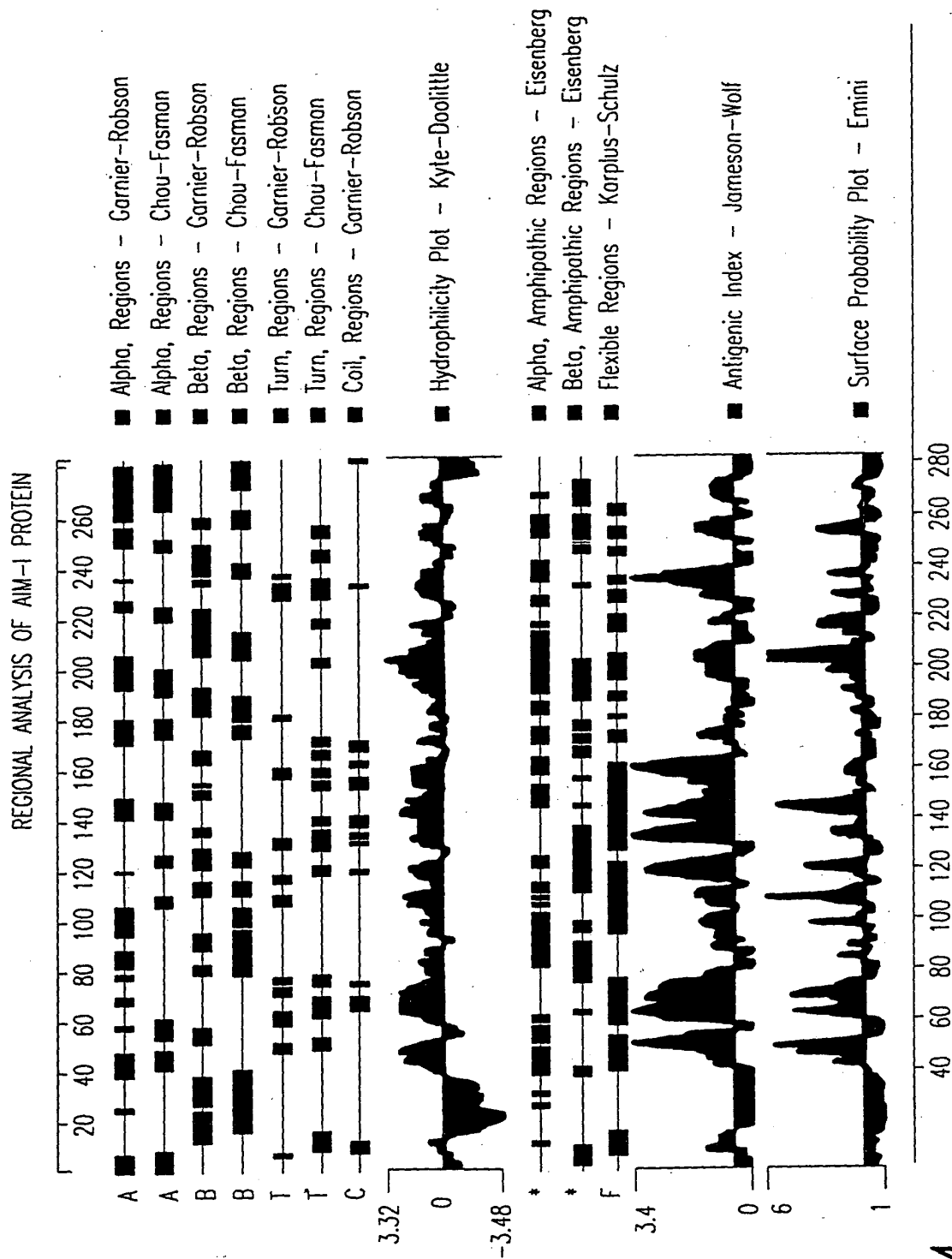


FIG. 4